

GNE.2630P1C11



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Ashkenazi et al. ) Group Art Unit Unknown  
App. No. : 09/978,295 )  
Filed : October 15, 2001 )  
For : SECRETED AND )  
TRANSMEMBRANE )  
POLYPEPTIDES AND )  
NUCLEIC ACIDS ENCODING )  
THE SAME )  
Examiner : Unknown )

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SUPPLEMENTAL INFORMATION DISCLOSURE STATEMENT

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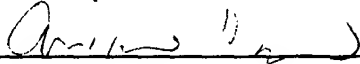
Dear Sir:

Enclosed is form PTO-1449 listing 2 references that are also enclosed. This Information Disclosure Statement is being filed before the receipt of a first Office Action on the merits, and presumably no fee is required in accordance with 37 C.F.R. § 1.97(b)(3). If a first Office Action on the merits was mailed before the mailing date of this Statement, the Commissioner is authorized to charge the fee set forth in 37 C.F.R. § 1.17(p) to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: April 30, 2002

By:   
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FORM PTO-1449

U.S. DEPARTMENT OF COMMERCE  
PATENT AND TRADEMARK OFFICEATTY. DOCKET NO.  
GNE 2630P1C11APPLICATION NO.  
09/978,295INFORMATION DISCLOSURE STATEMENT  
BY APPLICANT

(USE SEVERAL SHEETS IF NECESSARY)

APPLICANT  
Ashkenazi et al.FILING DATE  
October 15, 2001GROUP  
Unknown

EXAMINER INITIAL	OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PERTINENT PAGES, ETC.)
	1. Blast Results A1-A10 (Alignment of DNA40571 and various nucleotide sequences - GenBank Database), October 4, 2001
	2. Blast Results B1-B2 (Alignment of DNA40571 and various polypeptide sequences - Dayhoff Database), October 3, 2001

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Thu Oct 4 09:05:04 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]  
 /home/ruby/va/Molbio/carpanda/temp4/ss.DNA40571 (2365 bp)

Sequences producing High-scoring Segment Pairs:		Frame	Score	Match	Pct	E-val
1	P_AAA37664 Human peptidase, HPEP-8 coding sequence.	+	1334	1340	100	0.0
2	P_AAF30189 Clone 11618130.0.27 encoding secreted pr	+	1321	1345	99	0.0
3	AX079872 Sequence 3 from Patent WO0105971.	+	1321	1345	99	0.0
4	P_AAF30195 Clone 11618130.0.184 encoding secreted p	+	762	765	100	0.0
5	AX079884 Sequence 15 from Patent WO0105971.	+	762	765	100	0.0

>1 P\_AAA37664 Human peptidase, HPEP-8 coding sequence. DNA, PAT 24-OCT-2000  
 (1661 bp) [2 segs]  
 Score = 1334 (2644 bits), Expect = 0.0 [P\_AAA37664, seg 1/2]  
 Identities = 1340/1342 (99%), at 1010,320-2351,1661, Strand +/+

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DNA40571 1010 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTTCAGGCT
*****
P_AAA37664 320 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTTCAGGCT

DNA40571 1070 GGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAAC
*****
P_AAA37664 380 GGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAAC

DNA40571 1130 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCTGGCCAG
*****
P_AAA37664 440 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCTGGCCAG

DNA40571 1190 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG
*****
P_AAA37664 500 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG

DNA40571 1250 ACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC
*****
P_AAA37664 560 ACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC

DNA40571 1310 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGTCAGAGGAGGCGGTGCTAACTGCTGCC
*****
P_AAA37664 620 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGTCAGAGGAGGCGGTGCTAACTGCTGCC

DNA40571 1370 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG
*****
P_AAA37664 680 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG

DNA40571 1430 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG
*****

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P\_AAA37664 740 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC  
DNA40571 1490 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC  
\*\*\*\*\*  
P\_AAA37664 800 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC  
DNA40571 1550 CTCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTCTCTGGGA  
\*\*\*\*\*  
P\_AAA37664 860 CTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTCTCTGGGA  
DNA40571 1610 CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG  
\*\*\*\*\*  
P\_AAA37664 920 CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG  
DNA40571 1670 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG  
\*\*\*\*\*  
P\_AAA37664 980 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG  
DNA40571 1730 GGGATGGTGTGTACCAAGTGTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCA  
\*\*\*\*\*  
P\_AAA37664 1040 GGGATGGTGTGTACCAAGTGTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCA  
DNA40571 1790 CCACTGGTGCATGAGGTGAGGGGCACATGGTTCTTGCCGGGGCTGCACAGCTTCGGAGAT  
\*\*\*\*\*  
P\_AAA37664 1100 CCACTGGTGCATGAGGTGAGGGGCACATGGTTCTTGCCGGGGCTGCACAGCTTCGGAGAT  
DNA40571 1850 GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG  
\*\*\*\*\*  
P\_AAA37664 1160 GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG  
DNA40571 1910 GTCAGCAGTTTGGACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCCGAGGCTGAGCCT  
\*\*\*\*\*  
P\_AAA37664 1220 GTCAGCAGTTTGGACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCCGAGGCTGAGCCT  
DNA40571 1970 GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC  
\*\*\*\*\*  
P\_AAA37664 1280 GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC  
DNA40571 2030 TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCCTGTCTCCCCACCCTGT  
\*\*\*\*\*  
P\_AAA37664 1340 TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCCTGTCTCCCCACCCTGT  
DNA40571 2090 CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT  
\*\*\*\*\*  
P\_AAA37664 1400 CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT  
DNA40571 2150 GCCTGGGGCCACAGGTGCCCCACTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC  
\*\*\*\*\*  
P\_AAA37664 1460 GCCTGGGGCCACAGGTGCCCCACTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC  
DNA40571 2210 CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCCTTTACTCTTTCAGA  
\*\*\*\*\*  
P\_AAA37664 1520 CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCCTTTACCCTTTCAGA  
DNA40571 2270 TACAATCACGCCAGCCACGTTGTTTTGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTCC  
\*\*\*\*\*  
P\_AAA37664 1580 TACAATCACGCCAGCCACGTTGTTTTGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTCC

DNA40571 2330 TTTTTTTAACTTAAATAAATT  
 \*\*\*\*\*  
 P\_AAA37664 1640 TTTTTTTAACTTAAATAAATT

Score = 170 (337 bits), Expect = 8e-89 [P\_AAA37664, seg 2/2]  
 Identities = 170/170 (100%), at 844,1-1013,170, Strand +/+

DNA40571 844 GGACACCAGTGATGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCC  
 \*\*\*\*\*  
 P\_AAA37664 1 GGACACCAGTGATGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCC  
  
 DNA40571 904 CACATGTAAGTGTATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCC  
 \*\*\*\*\*  
 P\_AAA37664 61 CACATGTAAGTGTATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCC  
  
 DNA40571 964 TGGGATGCTATGTGGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG  
 \*\*\*\*\*  
 P\_AAA37664 121 TGGGATGCTATGTGGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG

>2 P\_AAF30189 Clone 11618130.0.27 encoding secreted protein SECP2. (1894 bp) [3  
 segs]

Score = 1321 (2619 bits), Expect = 0.0 [P\_AAF30189, seg 1/3]  
 Identities = 1345/1353 (99%), at 1010,534-2362,1886, Strand +/+

DNA40571 1010 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT  
 \*\*\*\*\*  
 P\_AAF30189 534 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT  
  
 DNA40571 1070 GGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAAC  
 \*\*\*\*\*  
 P\_AAF30189 594 GGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAAC  
  
 DNA40571 1130 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAG  
 \*\*\*\*\*  
 P\_AAF30189 654 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAG  
  
 DNA40571 1190 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG  
 \*\*\*\*\*  
 P\_AAF30189 714 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG  
  
 DNA40571 1250 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC  
 \*\*\*\*\*  
 P\_AAF30189 774 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC  
  
 DNA40571 1310 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTGCTGCC  
 \*\*\*\*\*  
 P\_AAF30189 834 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTGCTGCC  
  
 DNA40571 1370 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG  
 \*\*\*\*\*  
 P\_AAF30189 894 CACTGCTTCAATGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG  
  
 DNA40571 1430 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC  
 \*\*\*\*\*  
 P\_AAF30189 954 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC

DNA40571 1490 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC  
\*\*\*\*\*  
P\_AAF30189 1014 TACGACATGGCCCTCCTGCTGCTGGCTCAGCCTGTGACACTGGGAGCCAGCCTGCGGGCC  
  
DNA40571 1550 CTCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTCTCTGGGA  
\*\*\*\*\*  
P\_AAF30189 1074 CTCTGCCTGCCCTATTTTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTCTCTGGGA  
  
DNA40571 1610 CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG  
\*\*\*\*\*  
P\_AAF30189 1134 CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG  
  
DNA40571 1670 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG  
\*\*\*\*\*  
P\_AAF30189 1194 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG  
  
DNA40571 1730 GGGATGGTGTGTACCAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCA  
\*\*\*\*\*  
P\_AAF30189 1254 GGGATGGTGTGTACCAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCA  
  
DNA40571 1790 CCACTGGTGCATGAGGTGAGGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGAT  
\*\*\*\*\*  
P\_AAF30189 1314 CCACTGGTGCATGAGGTGAGGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGAT  
  
DNA40571 1850 GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG  
\*\*\*\*\*  
P\_AAF30189 1374 GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG  
  
DNA40571 1910 GTCAGCAGTTTGGACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCT  
\*\*\*\*\*  
P\_AAF30189 1434 GTCAGCAGTTTGGACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCT  
  
DNA40571 1970 GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC  
\*\*\*\*\*  
P\_AAF30189 1494 GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC  
  
DNA40571 2030 TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTGTCTCTCCCCACCCTGT  
\*\*\*\*\*  
P\_AAF30189 1554 TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTGTCTCTCCCCACCCTGT  
  
DNA40571 2090 CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT  
\*\*\*\*\*  
P\_AAF30189 1614 CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT  
  
DNA40571 2150 GCCTGGGGCCACAGGTGCCCCCTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC  
\*\*\*\*\*  
P\_AAF30189 1674 GCCTGGGGCCACAGGTGCCCCCTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC  
  
DNA40571 2210 CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCCTTTACTCTTTTCTCAGA  
\*\*\*\*\*  
P\_AAF30189 1734 CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCCTTTACCTTTTCTCAGA  
  
DNA40571 2270 TACAATCACGCCAGCCACGTTGTTTTGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCC  
\*\*\*\*\*  
P\_AAF30189 1794 TACAATCACGCCAGCCCCGTTGTTTTGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCC  
  
DNA40571 2330 TTTTTTTAACTTAAATAAATTGTTACAAAATA

\*\*\*\*\*  
P\_AAF30189 1854 TTTTAACTTAAATAAATTGTTACAAAATA

Score = 157 (311 bits), Expect = 5e-81 [P\_AAF30189, seg 2/3]  
Identities = 157/157 (100%), at 857,228-1013,384, Strand +/+

```
DNA40571 857 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT
*****
P_AAF30189 228 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT

DNA40571 917 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT
*****
P_AAF30189 288 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT

DNA40571 977 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCCTGTCAGG
*****
P_AAF30189 348 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCCTGTCAGG
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Score = 87 (172 bits), Expect = 3e-39 [P\_AAF30189, seg 3/3]  
Identities = 87/87 (100%), at 771,1-857,87, Strand +/+

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DNA40571 771 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA
*****
P_AAF30189 1 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA

DNA40571 831 CTGGCTGGGATCAGGACACCAGTGATG
*****
P_AAF30189 61 CTGGCTGGGATCAGGACACCAGTGATG
```

>3 AX079872 Sequence 3 from Patent WO0105971. (1894 bp) [3 segs]  
Score = 1321 (2619 bits), Expect = 0.0 [AX079872, seg 1/3]  
Identities = 1345/1353 (99%), at 1010,534-2362,1886, Strand +/+

```
DNA40571 1010 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT
*****
AX079872 534 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT

DNA40571 1070 GGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGTGCTGCTGACCAAC
*****
AX079872 594 GGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGTGCTGCTGACCAAC

DNA40571 1130 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCCAG
*****
AX079872 654 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCCAG

DNA40571 1190 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG
*****
AX079872 714 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG

DNA40571 1250 ACAGCAGGTCCCCAGGCAGGAGACCCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC
*****
AX079872 774 ACAGCAGGTCCCCAGGCAGGAGACCCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC

DNA40571 1310 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTGCTGCC
*****
AX079872 834 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTGCTGCC
```

DNA40571	1370	CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG *****
AX079872	894	CACTGCTTCAATGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG
DNA40571	1430	GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC *****
AX079872	954	GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC
DNA40571	1490	TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGGCC ***** **
AX079872	1014	TACGACATGGCCCTCCTGCTGCTGGCTCAGCCTGTGACACTGGGAGCCAGCCTGCGGGCC
DNA40571	1550	CTCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGA *****
AX079872	1074	CTCTGCCTGCCCTATTTTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGA
DNA40571	1610	CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCCTCCTGGGG *****
AX079872	1134	CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCCTCCTGGGG
DNA40571	1670	CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG *****
AX079872	1194	CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG
DNA40571	1730	GGGATGGTGTGTACCAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCA *****
AX079872	1254	GGGATGGTGTGTACCAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCA
DNA40571	1790	CCACTGGTGCATGAGGTGAGGGGCACATGGTTCTTGCCGGGCTGCACAGCTTCGGAGAT *****
AX079872	1314	CCACTGGTGCATGAGGTGAGGGGCACATGGTTCTTGCCGGGCTGCACAGCTTCGGAGAT
DNA40571	1850	GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG *****
AX079872	1374	GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG
DNA40571	1910	GTCAGCAGTTTGGAAGTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCT *****
AX079872	1434	GTCAGCAGTTTGGAAGTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCT
DNA40571	1970	GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC *****
AX079872	1494	GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC
DNA40571	2030	TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTGTCTCCCCACCCTGT *****
AX079872	1554	TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTGTCTCCCCACCCTGT
DNA40571	2090	CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT *****
AX079872	1614	CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT
DNA40571	2150	GCCTGGGGCCACAGGTGCCCACTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC *****
AX079872	1674	GCCTGGGGCCACAGGTGCCCACTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC
DNA40571	2210	CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCTTTACTCTTTCAGA



```

*****
AX079872  1734 CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCCTTTACCCTTTTCAGA
DNA40571  2270 TACAATCACGCCAGCCACGTTGTTTTGAAAATTTCTTTTTTTTGGGGGGCAGCAGTTTTCC
*****
AX079872  1794 TACAATCACGCCAGCCCCGTTGTTTTGAAAATTTCTTTTTTTTGGGGGGCAGCAGTTTTCC
DNA40571  2330 TTTTTTTAACTTAAATAAATTGTTACAAAATA
*****
AX079872  1854 TTTTTTTAACTTAAATAAATTGTTACAAAATA

```

Score = 157 (311 bits), Expect = 5e-81 [AX079872, seg 2/3]  
Identities = 157/157 (100%), at 857,228-1013,384, Strand +/-

```

DNA40571  857 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT
*****
AX079872  228 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT
DNA40571  917 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT
*****
AX079872  288 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT
DNA40571  977 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG
*****
AX079872  348 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG

```

Score = 87 (172 bits), Expect = 3e-39 [AX079872, seg 3/3]  
Identities = 87/87 (100%), at 771,1-857,87, Strand +/-

```

DNA40571  771 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA
*****
AX079872   1 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA
DNA40571  831 CTGGCTGGGATCAGGACACCAAGTGATG
*****
AX079872   61 CTGGCTGGGATCAGGACACCAAGTGATG

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>4 P\_AAF30195 Clone 11618130.0.184 encoding secreted protein SECP8. (1445 bp) [3  
segs]

Score = 762 (1511 bits), Expect = 0.0 [P\_AAF30195, seg 1/3]  
Identities = 765/766 (99%), at 1010,534-1775,1299, Strand +/-

```

DNA40571  1010 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT
*****
P_AAF30195  534 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT
DNA40571  1070 GGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGTGCTGCTGACCAAC
*****
P_AAF30195  594 GGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGTGCTGCTGACCAAC
DNA40571  1130 ACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCCAG
*****
P_AAF30195  654 ACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCCAG
DNA40571  1190 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG
*****
P_AAF30195  714 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG

```

DNA40571 1250 ACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC  
 \*\*\*\*\*  
 P\_AAF30195 774 ACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC  
 DNA40571 1310 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC  
 \*\*\*\*\*  
 P\_AAF30195 834 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC  
 DNA40571 1370 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG  
 \*\*\*\*\*  
 P\_AAF30195 894 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG  
 DNA40571 1430 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC  
 \*\*\*\*\*  
 P\_AAF30195 954 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC  
 DNA40571 1490 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC  
 \*\*\*\*\*  
 P\_AAF30195 1014 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC  
 DNA40571 1550 CTCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGA  
 \*\*\*\*\*  
 P\_AAF30195 1074 CTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGA  
 DNA40571 1610 CGGGCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG  
 \*\*\*\*\*  
 P\_AAF30195 1134 CGGGCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG  
 DNA40571 1670 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG  
 \*\*\*\*\*  
 P\_AAF30195 1194 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG  
 DNA40571 1730 GGGATGGTGTGTACCAGTGTGTGGGTGAGCTGCCCAGCTGTGAGG  
 \*\*\*\*\*  
 P\_AAF30195 1254 GGGATGGTGTGTACCAGTGTGTGGGTGAGCTGCCCAGCTGTGAGG

Score = 157 (311 bits), Expect = 5e-81 [P\_AAF30195, seg 2/3]  
 Identities = 157/157 (100%), at 857,228-1013,384, Strand +/+

DNA40571 857 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACGT  
 \*\*\*\*\*  
 P\_AAF30195 228 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACGT  
 DNA40571 917 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT  
 \*\*\*\*\*  
 P\_AAF30195 288 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT  
 DNA40571 977 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCTGTCAGG  
 \*\*\*\*\*  
 P\_AAF30195 348 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCTGTCAGG

Score = 87 (172 bits), Expect = 3e-39 [P\_AAF30195, seg 3/3]  
 Identities = 87/87 (100%), at 771,1-857,87, Strand +/+

DNA40571 771 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA  
 \*\*\*\*\*

P\_AAF30195 1 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA  
DNA40571 831 CTGGCTGGGATCAGGACACCAGTGATG  
\*\*\*\*\*  
P\_AAF30195 61 CTGGCTGGGATCAGGACACCAGTGATG

>5 AX079884 Sequence 15 from Patent W00105971. (1445 bp) [3 segs]  
Score = 762 (1511 bits), Expect = 0.0 [AX079884, seg 1/3]  
Identities = 765/766 (99%), at 1010,534-1775,1299, Strand +/+

DNA40571 1010 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT  
\*\*\*\*\*  
AX079884 534 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT  
DNA40571 1070 GGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGTGCTGCTGACCAAC  
\*\*\*\*\*  
AX079884 594 GGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGTGCTGCTGACCAAC  
DNA40571 1130 ACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAG  
\*\*\*\*\*  
AX079884 654 ACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAG  
DNA40571 1190 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG  
\*\*\*\*\*  
AX079884 714 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG  
DNA40571 1250 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC  
\*\*\*\*\*  
AX079884 774 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC  
DNA40571 1310 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC  
\*\*\*\*\*  
AX079884 834 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC  
DNA40571 1370 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG  
\*\*\*\*\*  
AX079884 894 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG  
DNA40571 1430 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC  
\*\*\*\*\*  
AX079884 954 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC  
DNA40571 1490 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC  
\*\*\*\*\*  
AX079884 1014 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC  
DNA40571 1550 CTCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCCTGGGA  
\*\*\*\*\*  
AX079884 1074 CTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCCTGGGA  
DNA40571 1610 CGGGCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGGCCGTGACCCTCCTGGGG  
\*\*\*\*\*  
AX079884 1134 CGGGCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGGCCGTGACCCTCCTGGGG  
DNA40571 1670 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG  
\*\*\*\*\*  
AX079884 1194 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG

DNA40571 1730 GGGATGGTGTGTACCAAGTGTGTGGGTGAGCTGCCCAGCTGTGAGG  
\*\*\*\*\*  
AX079884 1254 GGGATGGTGTGTACCAAGTGTGTGGGTGAGCTGCCCAGCTGTGAGG

Score = 157 (311 bits), Expect = 5e-81 [AX079884, seg 2/3]  
Identities = 157/157 (100%), at 857,228-1013,384, Strand +/+

DNA40571 857 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT  
\*\*\*\*\*  
AX079884 228 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT  
  
DNA40571 917 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT  
\*\*\*\*\*  
AX079884 288 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT  
  
DNA40571 977 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG  
\*\*\*\*\*  
AX079884 348 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG

Score = 87 (172 bits), Expect = 3e-39 [AX079884, seg 3/3]  
Identities = 87/87 (100%), at 771,1-857,87, Strand +/+

DNA40571 771 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA  
\*\*\*\*\*  
AX079884 1 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA  
  
DNA40571 831 CTGGCTGGGATCAGGACACCAAGTGATG  
\*\*\*\*\*  
AX079884 61 CTGGCTGGGATCAGGACACCAAGTGATG

Wed Oct 3 10:32:47 2001 [BLASTP 2.2.1 [Jul-12-2001], NCBI]  
/home/ruby/va/Molbio/carpenda/new.pro/pl.DNA40571.nc (347 aa)

Sequences producing High-scoring Segment Pairs:				Score	Match	Pct	E-val
1	P_AAB24046	Human PRO351 protein sequence	SEQ ID NO:1	1897	347	100	0.0
2	P_AAB44260	Human PRO351 (UNQ308) protein sequence	SE	1897	347	100	0.0
3	P_AAY41704	Human PRO351 protein sequence	- Homo sapi	1897	347	100	0.0

>1 P\_AAB24046 Human PRO351 protein sequence SEQ ID NO:12 - Homo sapiens. (571 aa) [2 segs]

Score = 1897 (735 bits), Expect = 0.0 [P\_AAB24046, seg 1/2]  
Identities = 347/347 (100%), Positives = 347/347 (100%), at 1,225-347,571

DNA40571.nc	1	MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS
		*****
P_AAB24046	225	MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS
DNA40571.nc	61	WLQARVQGAAFLAQSPETPEMSDEDSVACGSLRTAGPQAGAPSPWPWEARLMHQQLAC
		*****
P_AAB24046	285	WLQARVQGAAFLAQSPETPEMSDEDSVACGSLRTAGPQAGAPSPWPWEARLMHQQLAC
DNA40571.nc	121	GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL
		*****
P_AAB24046	345	GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL
DNA40571.nc	181	LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPTLLGPRACSR
		*****
P_AAB24046	405	LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPTLLGPRACSR
DNA40571.nc	241	LHAAPGGDGSPIPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSGFDACQGPA
		*****
P_AAB24046	465	LHAAPGGDGSPIPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSGFDACQGPA
DNA40571.nc	301	RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC
		*****
P_AAB24046	525	RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC

>2 P\_AAB44260 Human PRO351 (UNQ308) protein sequence SEQ ID NO:132 - Homo (571 aa) [2 segs]

Score = 1897 (735 bits), Expect = 0.0 [P\_AAB44260, seg 1/2]  
Identities = 347/347 (100%), Positives = 347/347 (100%), at 1,225-347,571

DNA40571.nc	1	MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS
		*****
P_AAB44260	225	MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS
DNA40571.nc	61	WLQARVQGAAFLAQSPETPEMSDEDSVACGSLRTAGPQAGAPSPWPWEARLMHQQLAC
		*****

```
P_AAB44260 285 WLQARVQGAAFLAQSPETPEMSDEEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLAC
DNA40571.nc 121 GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL
*****
P_AAB44260 345 GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL
DNA40571.nc 181 LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPVTLTGPRACSR
*****
P_AAB44260 405 LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPVTLTGPRACSR
DNA40571.nc 241 LHAAPGGDGSPIPLPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPA
*****
P_AAB44260 465 LHAAPGGDGSPIPLPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPA
DNA40571.nc 301 RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEFGSCLANISQPTSC
*****
P_AAB44260 525 RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEFGSCLANISQPTSC
```

>3 P\_AAY41704 Human PRO351 protein sequence - Homo sapiens. (571 aa) [2 segs]  
Score = 1897 (735 bits), Expect = 0.0 [P\_AAY41704, seg 1/2]  
Identities = 347/347 (100%), Positives = 347/347 (100%), at 1,225-347,571

```
DNA40571.nc 1 MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS
*****
P_AAY41704 225 MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS
DNA40571.nc 61 WLQARVQGAAFLAQSPETPEMSDEEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLAC
*****
P_AAY41704 285 WLQARVQGAAFLAQSPETPEMSDEEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLAC
DNA40571.nc 121 GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL
*****
P_AAY41704 345 GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL
DNA40571.nc 181 LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPVTLTGPRACSR
*****
P_AAY41704 405 LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPVTLTGPRACSR
DNA40571.nc 241 LHAAPGGDGSPIPLPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPA
*****
P_AAY41704 465 LHAAPGGDGSPIPLPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPA
DNA40571.nc 301 RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEFGSCLANISQPTSC
*****
P_AAY41704 525 RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEFGSCLANISQPTSC
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